

FIGURE 1A

ATGGAGAGCAAGGTGCTGCTGGCCGTCGCCCTGTGGCTCTGCGTGGAGACCC
 GGGCCGCCTCTGTGGGTTTGCCTAGTGTCTCTTGATCTGCCCAGGCTCAGCA
 TACAAAAAGACATACTTACAATTAAGGCTAATACTCAACTCTTCAAATTACTTGCAG
 GGGACAGAGGGGACTTGGACTGGCTTTGGCCCAATAATCAGAGTGGCAGTGAG
 CAAAGGGTGGAGGTGACTGAGTGCAGCGATGGCCTCTTCTGTAAGACACTCAC
 AATTCCAAAAGTGATCGGAAATGACACTGGAGCCTACAAGTGCTTCTACCGGG
 AAAGTGAAGTGGCCTCGGTCAATTTATGTCTATGTTCAAGATTACAGATCTCCATT
 TATTGCTTCTGTAGTGACCAACATGGAGTCGTGTACATTACTGAGAACAAAA
 CAAAAGTGTGGTGATTCCATGTCTCGGGTCCATTTCAAATCTCAACGTGTCACTT
 TGTGCAAGATACCCAGAAAAGAGATTTGTTCTGATGGTAACAGAAATTTCTGG
 GACAGCAAGAAGGGCTTTACTATTCCAGCTAGATGATCAGCTATGCTGGCATG
 GTCTTCTGTGAAGCAAAAATTAATGATGAAAGTTACCAGTCTATTATGTACATAG
 TTGTCGTTGTAGGGTATAGGATTTATGATGTGGTTCTGAGTCCGTCTCATGGAA
 TTGAAGTATCTGTTGGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAAC
 TAAATGTGGGGATTGACTTCAACTGGGAATACCTTCTTTCGAAGCATCAGCATA
 AGAAACTTGTAAACCGAGACCTAAAAACCCAGTCTGGGAGTGAGATGAAGAAA
 TTTTGTAGCACCTTAAGTATAGATGGTGTAAACCCGGAGTGACCAAGGATTGTAC
 ACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACAGCACATTTGTGAG
 GGTCCATGAAAAACCTTTTGTGCTTTTGGAAAGTGGCATGGAATCTCTGGTGGA
 AGCCACGGTGGGGGAGCGTGTGAGAATCCCTGCGAAGTACCTTGGTTACCCAC
 CCCAGAAATAAAATGGTATAAAATGGAATACCCCTTGAGTCCAATCACACAA
 TTAAGCGGGGCATGTAAGTACGATTATGGAAGTGAGTGAAAGAGACACAGGA
 AATTACAGTGTCACTCTTACCAATCCCATTTCAAAGGAGAAGCAGAGCCATGTG
 GTCTCTCTGGTTGTGTATGTCCACCCAGATTGGTGAGAAATCTCTAATCTCTC
 CTGTGGATTCTTACCAGTACGGCACCACTCAAACGCTGACATGTACGGTCTATG
 CCATTCTCCCCCGCATCACATCCACTGGTATTGGCAGTTGGAGGAAGAGTGC
 GCCAACGAGCCCAGCCAAGCTGTCTCAGTGACAAACCCATACCTTGTGAAGA
 ATGGAGAAGTGTGGAGGACTTCCAGGGAGGAAATAAAATTGAAGTTAATAAAA
 ATCAATTTGCTCTAATTGAAGGAAAAAACAACCTGTAAGTACCTTGTATCCA
 AGCGGCAAATGTGTCAGCTTTGTACAAATGTGAAGCGGTCAACAAAGTCGGGA
 GAGGAGAGAGGGTGATCTCCTTCCACGTGACCAGGGGTCTGAAATTAATTTG
 CAACCTGACATGCAGCCCACTGAGCAGGAGAGCGTGTCTTTGTGGTGCACCTGC
 AGACAGATCTACGTTTGAGAACCTCACATGGTACAAGCTTGGCCACAGCCTCT
 GCCAATCCATGTGGGAGAGTTGCCACACCTGTTTGCAAGAACTTGGATACTCT
 TTGGAAATTGAATGCCACCATGTTCTCTAATAGCACAAATGACATTTTGATCATG
 GAGCTTAAGAATGCATCCTTGCAAGGACCAAGGAGACTATGTCTGCCTTGCA
 GACAGGAAGAACCAAGAAAGACATTGCGTGGTTCAGGCAGCTCACAGTCCTAGA
 GCGTGTGGCACCCACGATCACAGGAAACCTGGAGAATCAGACGACAAGTATTG
 GGGAAAGCATCGAAGTCTCATGCACGGCATCTGGGAATCCCCCTCCACAGATC
 ATGTGGTTTAAAGATAATGAGACCTTGTAGAAGACTCAGGCATTGTATTGAAG
 GATGGGAACCGGAACCTCACTATCCGCAGAGTGAGGAAGGAGGACGAAGGCC
 TCTACACCTGCCAGGCATGCAGTGTCTTGGCTGTGCAAAAGTGGAGGCATTTT
 TCATAATAGAAGGTGCCAGGAAAAGACGAACCTTGGAATCATTATTCTAGTAG
 GCACGGCGGTGATTGCCATGTTCTTCTGGCTACTTCTTGTTCATCATCTACGGA
 CCGTTAAGCGGGCCAATGGAGGGGAACCTGAAGACAGGGTACCTGTCCATCGT
 CATGGACCCAGATGAACTCCCATTTGGATGAACATTGTGAACGACTGCCTTATGA
 TGCCAGCAAATGGGAATTTCCCAAGAGACCGGCTGAAGCTAGGTAAGCCTCTTG
 GCCGTGGTGCCTTTGGCCAAGTGATTGAAGCAGATGCCTTTGGAATTGACAAG
 ACAGCAACTTGCAGGACAGTAGCAGTCAAAATGTTGAAAGAAGGAGCAACACA
 CAGTGAGCATCGAGCTCTCATGTCTGAACTCAAGATCCTCATTTCATTTGGTCA
 CCATCTCAATGTGGTCAACCTTCTAAGTGCCTGTACCAAGCCAGGAGGGCCAC
 TCAAGGTGAAATTGTGAAATTTGCAAAATTTGGAAACCTGTCCACTTACCTGAGGA
 GCAAGAGAAATGAATTGTCCCTACAAGACCAAGGGGCACGATTCCGTCAA
 GGGAAAGACTACGTTGGAGCAATCCCTGTGGATCTGAAACGGCGCTTGGACAG

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FIGURE 1B

CATCACCAGTAGCCAGAGCTCAGCCAGCTCTGGATTTGTGGAGGAGAAGTCCC
TCAGTGATGTAGAAGAAGAGGAAGCTCCTGAAGATCTGTATAAGGACTTCCTG
ACCTTGGAGCATCTCATCTGTTACAGCTTCCAAGTGGCTAAGGGCATGGAGTTC
TTGGCATCGCGAAAGTGTATCCACAGGGACCTGGCGGCACGAAATATCCTCTT
ATCGGAGAAGAACGTGGTTAAAATCTGTGACTTTGGCTTGGCCCGGGATATTTA
TAAAGATCCAGATTATGTCAGAAAAGGAGATGCTCGCCTCCCTTTGAAATGGAT
GGCCCCAGAAACAATTTTGTACAGAGTGTACACAATCCAGAGTGACGTCTGGT
CTTTTGGTGTTTTGTGTGGGAAATATTTTCTTAGGTGCTTCTCCATATCCTGG
GGTAAAGATTGATGAAGAATTTTGTAGGCGATTGAAAGAAGGAACTAGAATGA
GGGCCCCCTGATTATACTACACCAGAAATGTACCAGACCATGCTGGACTGCTGG
CACGGGGAGCCCAGTCAGAGACCCACGTTTTTCAGAGTTGGTGGAAACATTTGGG
AAATCTCTTGCAAGCTAATGCTCAGCAGGATGGCAAAGACTACATTGTTCTTCC
GATATCAGAGACTTTGAGCATGGAAGAGGATTCTGGACTCTCTCTGCCTACCTC
ACCTGTTTCTGTATGGAGGAGGAGGAAGTATGTGACCCCAAATTCATTATGA
CAACACAGCAGGAATCAGTCAGTATCTGCAGAACAGTAAGCGAAAGAGCCGGC
CTGTGAGTGTAAAAACATTTGAAGATATCCCGTTAGAAGAACCAGAAGTAAAAG
TAATCCCAGATGACAACCAGACGGACAGTGGTATGGTTCCTTGCCTCAGAAGAG
CTGAAAACCTTTGGAAGACAGAACCAAATTATCTCCATCTTTTGGTGGAAATGGT
CCCAGCAAAGCAGGGAGTCTGTGGCATCTGAAGGCTCAAACCAGACAAGCG
GCTACCAGTCCGGATATCACTCCGATGACACAGACACCACCGTGTACTCCAGT
GAGGAAGCAGAACTTTTAAAGCTGATAGAGATTGGAGTGCAAACCGGTAGCAC
AGCCCAGATTCTCCAGCCTGACTCGGGGACCACACTGAGCTCTCCTCCTGTTTA
A

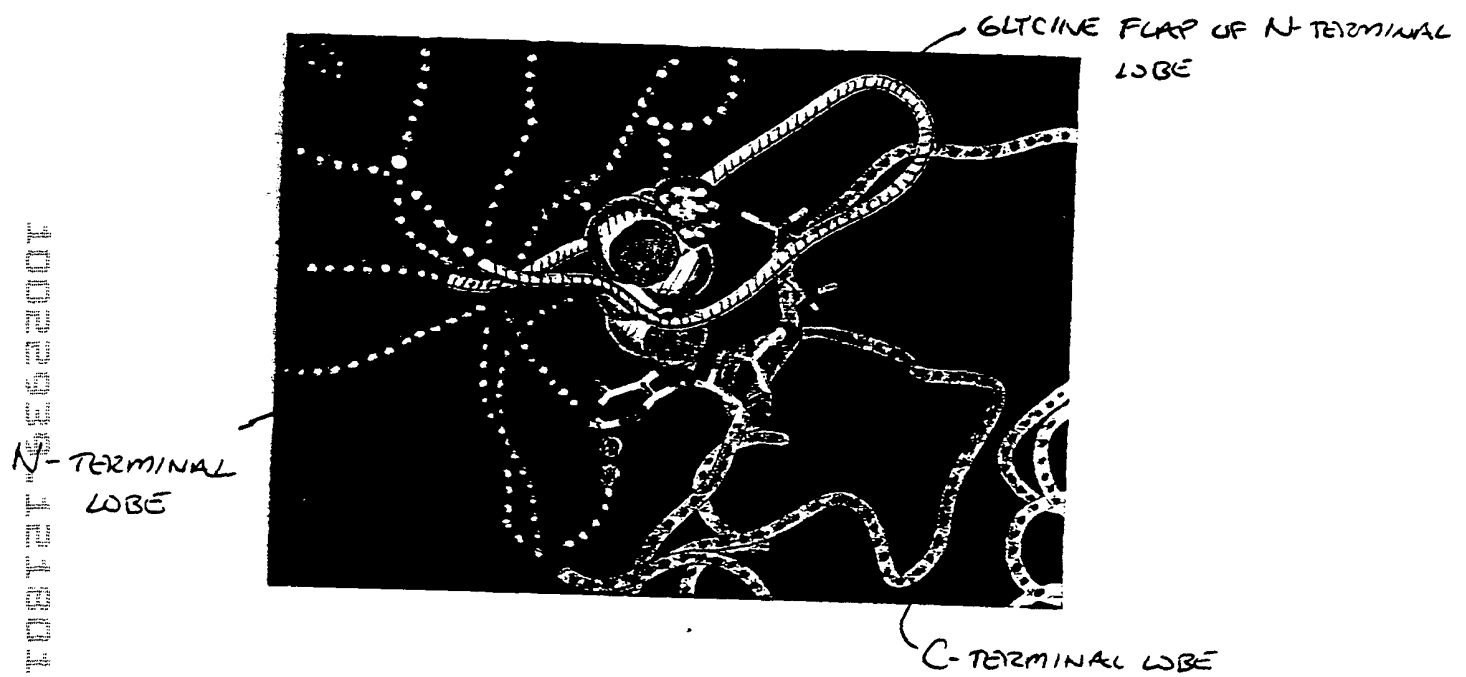
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FIGURE 2

MESKVLLAVALWLCVETRAASVGLPSVSLDLPRLSIQKDILTIKANTTLQITCRGQR
DLDWLWPNNQSGSEQRVEVTECSDGLFCKLTIPKVIGNDTGAYKCFYRETDLAS
VTYVYVQDYRSPFLASVSDQHGVVYTENKNKTVVIPCLGSIENLVSLCARYPEKR
FVPDGNRISWDSKKGFTIPSYMISYAGMVFCFAKINDESYQSIMYTVVVVGYRIYDV
VLSPSHGIELSVGEKLVNCTARTELVNVIDFNWEYPSSKHQHKLVNRDLKTQS
GSEMKKFLSTLTIDGVTRSDQGLYTCAASSGLMTKKNSTFVRVHEKPFVAFGSGM
ESLVEATVGERVRIPAKYLGYPPEIKWYKNGIPLESNHTIKAGHVLTMEVSEKDT
GNYTVILTNPISKEKQSHVVSLVYVPPQIGESLISPVDSYQYGTQTTLCTVYAI
PPHHIHWYWQLEEECANEPSQAVSVTNYPCEEWRVSEDFQGGNKIEVNKNQFA
LIEGKNKTVSTLVIQAANVSALYKCEAVNKVGRGERVISFHVTRGPEITLQPDMP
TEQESVSLWCTADRSTFENLTWYKLGPOPLPHVGEPLTPVCKNLDTLWKLNATM
FSNSTNDILMELKNASLQDQGDYVCLAQDRKTKKRHCVRQLTVLERVAPTITGN
LENQTTSIGESIEVSCASGNPPQIMWFKDNETLVEDSGIVLKDGNRNLTIRRVK
EDEGLYTCQACSVLGCAKVEAFFIEGAQEKTNLEIILVGTAVIAMFFWLLLVIILRT
VKRANGGELKTGYLSIVMDPDELPLDEHCERLPYDASKWEFPRDRLKLGKPLGRG
AFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHILNVV
NLLGACTKPGGPLMVTEVECKFGNLSTYLRSKRNEFVPYKTKGARFRQGDYVG
APVDLKRRLDSITSSQSSASSGFVEEKSLSDVEEEEAPEDLYKDFTLEHLICYSFQ
VAKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDAR
LPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGT
RMRAPDYTTPEMYQTMLDCTWHGEPSQRPTFSELVEHLGNLLQANAQQDGKDYTVL
PISETLSMEEDSGLSLPTSPVSCMEEEEVCDPKFHYDNTAGISQYLQNSKRKSRPVS
VKTFEDIPLEPEVKVIPDDNQTDSGMVLASEELKTLEDRTKLSPSFGGMVPSKSRE
SVASEGSNQTSQYQSGYHSDDTDTTVYSSEEAEILLKLEIGVQTGSTAQILQPDSTGT
TLSSPPV

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FIGURE 3A



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FIGURE 3B

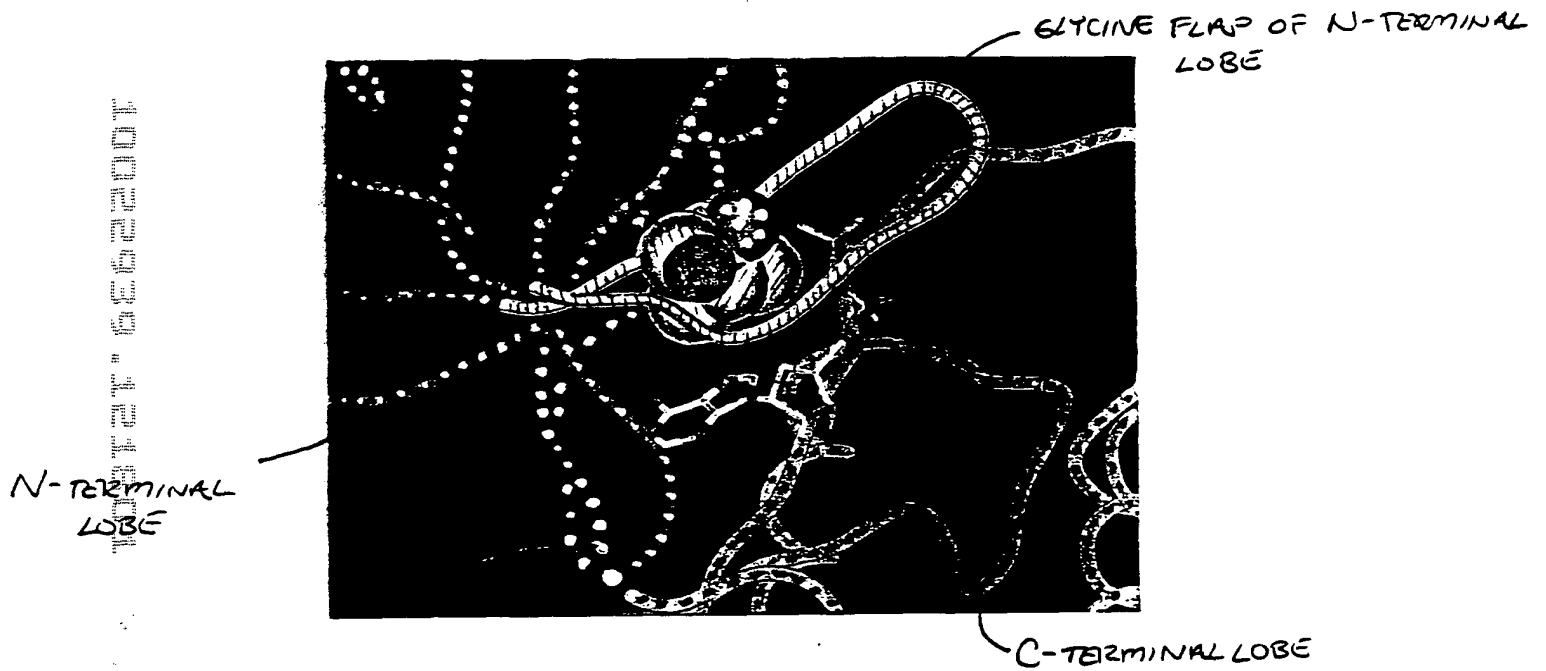


FIGURE 4A

Anti-phosphotyrosine

E848 V848

12	12	120	12
-	+	+	-

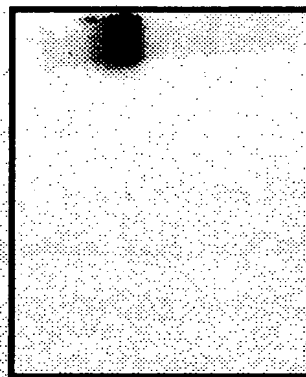


FIGURE 4B

Anti-KDR

E848 V848

120	12
-	-

Enzyme (ng)
ATP (1 mM)

